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U.S. ARMY CHEMICAL AND BIOLOGICAL DEFENSE COMMAND

ERDEC-TR-461

**USING SEQUENCE ANALYSIS
TO IDENTIFY CULTURES DERIVED FROM AIRBORNE SPORES**

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January 1998

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REPORT DOCUMENTATION PAGE			Form Approved OMB No. 0704-0188	
Public reporting burden for this collection of information is estimated to average 1 hour per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden, to Washington Headquarters Services, Directorate for Information Operations and Reports, 1215 Jefferson Davis Highway, Suite 1204, Arlington, VA 22202-4302, and to the Office of Management and Budget, Paperwork Reduction Project (0704-0188), Washington, DC 20503.				
1. AGENCY USE ONLY (Leave Blank)		2. REPORT DATE 1998 January		3. REPORT TYPE AND DATES COVERED Final; 96 Jul - 97 Jul
4. TITLE AND SUBTITLE Using Sequence Analysis to Identify Cultures Derived from Airborne Spores			5. FUNDING NUMBERS PR-10262384A553	
6. AUTHOR(S) Wick, Charles H.; Yeh, Homer R. (ERDEC); Cline, Erica; and Edmonds, Robert L. (University of Washington)				
7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES) DIR, ERDEC, ATTN: SCBRD-RTE, APG, MD 21010-5423 University of Washington, Seattle, WA 98195			8. PERFORMING ORGANIZATION REPORT NUMBER ERDEC-TR-461	
9. SPONSORING/MONITORING AGENCY NAME(S) AND ADDRESS(ES)			10. SPONSORING/MONITORING AGENCY REPORT NUMBER	
11. SUPPLEMENTARY NOTES				
12a. DISTRIBUTION/AVAILABILITY STATEMENT Approved for public release; distribution is unlimited.			12b. DISTRIBUTION CODE	
13. ABSTRACT (Maximum 200 words) The purpose of this project was to evaluate rDNA sequencing in identifying airborne fungal spores. Universal fungal small-subunit (SSU) ribosomal RNA primers were used with the polymerase chain reaction (PCR) to amplify the SSU rRNA gene from each isolate for sequencing. Sequences were analyzed through the ribosomal database project to identify the most closely related known rDNA sequence. Restriction fragment length polymorphisms (RFLPs) were obtained from three cultures to be used to detect each culture in mixed samples. Of the five stock cultures studied, one common fungus could be identified to genus with some confidence (<i>Mucor</i>). For three cultures, sequence data yielded closest matches that were probably closely related genera (<i>Penicillium</i> , <i>Aureobasidium</i> , <i>Spongipellis</i>), but the phylogenetic tree lacked the resolution for genus identification, whereas sequence results from the one culture were more ambiguous. The RFLP analysis could detect the presence of some cultures in mixed DNA isolates, with varying degrees of sensitivity. Although there are not yet enough published sequences to identify less common airborne fungi using sequencing of the SSU rDNA gene, our results indicate that the molecular methods evaluated in this study could have the potential to identify fungal spores from common genera and detect them in mixed environmental samples.				
14. SUBJECT TERMS <i>Mucor</i> PCR <i>Penicillium</i> Airborne samples <i>Spongipellis</i> DNA fingerprinting <i>Aureobasidium</i> Polymerase chain reaction			15. NUMBER OF PAGES 31	
			16. PRICE CODE	
17. SECURITY CLASSIFICATION OF REPORT UNCLASSIFIED		18. SECURITY CLASSIFICATION OF THIS PAGE UNCLASSIFIED		19. SECURITY CLASSIFICATION OF ABSTRACT UNCLASSIFIED
			20. LIMITATION OF ABSTRACT UL	

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PREFACE

The work described in this report was authorized under Project No. 10262384A553, Non-Medical CB Defense. This work was started in July 1996 and completed in July 1997.

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CONTENTS

INTRODUCTION	7
METHODS	9
Stock Cultures	9
DNA Extraction	9
PCR Amplification of the SSU rRNA Gene and Sequencing	9
Analysis of Sequence Data	10
Molecular Markers (Restriction Fragment Length Polymorphisms, RFLPs)	10
RESULTS	11
Sequences and Direct Observations of Stock Cultures	11
Molecular Markers of Cultures 1, 2, and 3	13
DISCUSSION	16
Sequence Analysis	16
Molecular Markers for Detecting Previously Identified Organisms	17
LITERATURE CITED	19
APPENDIXES	
A. SEQUENCE OF CULTURES DATA	21
B. PICTURES OF STOCK CULTURES	27
C. BUFFERS	31

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USING SEQUENCE ANALYSIS TO IDENTIFY CULTURES DERIVED FROM AIRBORNE SPORES

INTRODUCTION

Many medically or ecologically significant microbes are spread predominantly through the air. These airborne microbes are of interest for a variety of reasons, including human, animal and plant health and forest ecology. The purpose of this study is to investigate methods of characterizing airborne biological particles, with the ultimate goal of developing real-time, culture free means of detecting and identifying unique particles. Flow cytometry, gas chromatography and molecular techniques were deemed to be the most promising techniques (Edmonds, 1994; Wick, *et al.*, 1994, 1995, 1997).

It was proposed that the detection of airborne biological particles could be based on their physical characteristics as detected by flow cytometer analysis and identification of biochemical profiles by gas chromatography. Initial research involving flow cytometry and gas chromatography were discussed in a previous report (Wick, *et al.*, 1997). A combination of gas chromatography and mass spectrometry has been used successfully to determine sugar composition in the walls of cysts of *Pneumocystis carinii* (DeStefano *et al.* 1990) and prespore specific antigens of a cellular slime mold *Dictyostelium discoideum* (Zachara *et al.* 1996).

Recently, our focus has been upon investigating molecular methods of identifying fungal airborne spores, to be used in combination with physical and biochemical techniques of characterizing field samples of airborne particles. The chief advantage of using a molecular approach is that it is possible to achieve a highly reliable and detailed identification of individual isolates. There are some significant challenges and limitations associated with molecular techniques. Published sequence databases are still quite limited, making it difficult to find a match, especially when studying fungi that are not medically significant; also, molecular techniques generally require a minimum of several days, although turn-around times are becoming increasingly rapid as the technology becomes more refined.

Molecular techniques can be quite powerful when used in combination with physical or chemical separation criteria. For example, real-time flow cytometry and gas chromatography could be used to produce biochemical profiles which would indicate the presence of an unusual biological particle. Molecular methods could then be used to determine the phylogenetic identity of the biological particle e.g., the most closely related known species. The power of this approach is that it can be used to study a completely unknown organism, without prior knowledge of its identity, and without the necessity of culturing it.

Molecular techniques have recently become common in the study of fungal systematics, resulting in the development of reliable protocols for DNA isolation from fungal cultures and analysis of molecular markers or sequence data. In particular, the ribosomal RNA genes have received considerable attention, resulting in development of an increasingly detailed phylogenetic tree based on sequence-level variation in the rRNA genes. As rRNA genes from more and more fungal species are sequenced, the expanding database becomes increasingly attractive as a tool for characterizing unknown cultures. Briefly, the typical approach is to isolate genomic DNA from the unknown culture (or single spore), amplify (copy) the rRNA gene using short DNA strands (18-20 nucleotides long) known as primers with the polymerase chain reaction (PCR), and then sequence the amplified rRNA gene. The sequence is aligned with rRNA sequences from known organisms, and the organism whose gene is most similar to the unknown's is identified.

In selecting a strategy, we needed to choose a gene for which reliable universal primers and an extensive database of fungal sequences had already been determined. Also, the sequence of the gene had to be variable enough to distinguish to the genus level. The small-subunit (SSU, or 18S) rDNA gene evolves relatively slowly, and is therefore useful for studying distantly related organisms (White *et al.*, 1990), and has been used by many researchers to study fungal phylogenetics (e.g. White *et al.*, 1990; Spatafora *et al.*, 1995). Therefore, we chose to evaluate sequencing of the SSU rDNA gene as a means of identifying fungal isolates from airborne spores.

To assess the feasibility of this approach, we began by working with stock cultures of fungi obtained from common airborne spores. Our objectives were: 1) to determine whether sequencing of the SSU rDNA gene could identify common airborne fungi at the genus level, and 2) to evaluate the use of molecular markers in detecting unique fungi after they had been identified by sequencing.

METHODS

Stock Cultures

The stock cultures discussed in this report were obtained in October 1993 from airborne spores collected on open agar plates from various locations on the University of Washington campus, and maintained in pure culture on agar slants. Cultures were inoculated onto thin films of agar under glass coverslips on microscope slides, grown at 22° C for 5-10 days, observed at 100x and 400x under a light microscope, and photographed. In addition, stock cultures were grown on agar plates, agar blocks were dissected out and placed on mounts for use in an environmental scanning electron microscope (SEM), and prints were made of characteristic features from each culture.

DNA Extraction

Genomic DNA was isolated according to a protocol provided by George Mueller (University of Washington, personal communication, 1996). Randomly selected cultures were inoculated in 0.5 ml of liquid medium in 1.5 ml epindorf tubes, and incubated at 22° C for 2 days. Hyphae were pelleted in a microcentrifuge at 12,000 rpm for 60 seconds, culture medium was decanted, and hyphae were rinsed once with sterile water. For samples in which the volume of the pellet exceeded approx. 25 µL, the excess volume was removed, and the pellet was washed again in sterile water. The sample was then immersed in liquid nitrogen to freeze, and ground to a fine powder with a sterile micropestle. Freezing and grinding was repeated once, 30 µL of 2x CTAB (Appendix C) was added, and the sample was mixed using the micropestle. Samples were frozen and thawed repeatedly (3x) in liquid nitrogen and a 65° C waterbath. Samples were incubated in a 65° C water bath for one hour. Proteins and other cell components were removed via chloroform extraction, and DNA was precipitated in isopropanol and washed in Wash Buffer (Appendix C) and 95% ethanol.

PCR Amplification of the SSU rRNA Gene and Sequencing

A 1150 bp fragment of the SSU rRNA gene was amplified using the universal primers NS1 and NS4 (Figure 1), which have been tested with a wide range of fungal species (White *et al.*, 1990). The reaction conditions were those used by Spatafora *et al.* (1995) with some modifications: 40 cycles of 94° C for 1 min., 53° C for 1 min., and 72° C for 1 min. Genomic DNA extracts were diluted in water at three serial dilutions: 1:100, 1:1000, and 1:10000. Successful amplification was detected on agarose gels. The DNA was purified using QiaQuick PCR purification columns (Qiagen), with a guanidine HCl

modification of the normal protocol to exclude primer dimers. The purified PCR product was submitted to the Biochemistry DNA sequencing facility at the University of Washington for sequence determination.

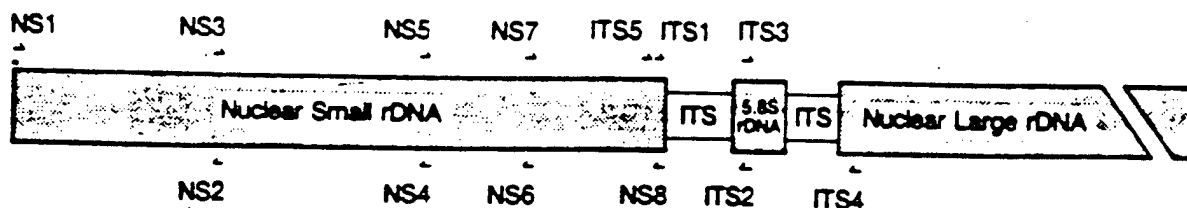


Figure 1: The Ribosomal DNA Gene Cluster and NS1 and NS4 Primers
(White *et al.*, 1990)

Analysis of Sequence Data

Sequences were determined in both directions using the NS1 and the NS4 primers, resulting in a region of overlap in the center of the approximately 1050 bp fragment of the SSU gene. Sequence results were confirmed by visual inspection of the sequencing gel readout, and ambiguous bases were designated as N. The sequence of the SSU rRNA gene from each of the selected cultures was compared with known SSU rRNA sequences in the Ribosomal Database Project database (Maidak *et al.*, 1996), resulting in a list of the most closely related sequences in the database and their similarity rank.

Molecular Markers (Restriction Fragment Length Polymorphisms, RFLP s)

For selected cultures, SSU rRNA genes were amplified by the PCR and the resulting amplified sequence was digested with one of two restriction enzymes: Cfo I and Hpa II in React 8 reaction buffer (Gibco BRL). In addition, genomic DNA extracts from each culture were mixed at 1:1 or 1:100 ratios with each of the other cultures to simulate the effect of isolating DNA from a mixed fungal sample. PCR was performed and the amplified product was digested with Cfo I and Hpa II, as previously described. Digested DNA was separated on an agarose gel, stained with ethidium bromide, and digitized by a video analyzer. Migration of each band was measured using NIH-Image software and gel measurement macros, and migration was quantified in reference to the 100 bp band of the 100 bp DNA ladder (Gibco BRL).

RESULTS

Sequences and Direct Observations of Stock Cultures

Sequences were obtained for five stock cultures (Appendix A). Photographs of light microscopy and environmental SEM results are presented in Appendix B. Culture 1 resembled *Penicillium*, but had long chains of conidia not typical of *Penicillium*. The sequence's closest match was *Penicillium notatum*, with a fairly low similarity rank of 0.749 (see Table 1 and Figure 2). The culture appeared to be in the *Penicillium/Aspergillus* cluster, but it could not be identified to genus. Culture 2 had sporangia characteristic of *Mucor*, and the closest matching sequence was *Mucor racemosus*, with a

Table 1. Sequence Analysis of Cultures Derived from Airborne Spores

Culture #	Closest Matches	Similarity Rank (RDP)	GCG-GAP Quality	Morphol. ID
1	<i>Penicillium notatum</i>	.749		Penicillium?
	<i>Aspergillus fumigatus</i>	.713		
2	<i>Mucor racemosus</i>	.881		Mucor
	<i>Endogone pisiformis</i>	.408		
3	<i>Aureobasidium pullulans</i>	.884		Aureobasidium?
	<i>Pleospora rudis</i>	.750		
4	<i>Spongipellis unicolor</i>	.807	1010.7	Heterobasidion?
	<i>Heterobasidion annosum</i> *		1008.7	
	<i>Thanatephorus praticola</i>	.765	966.9	
5	<i>Aureobasidium pullulans</i>	.831		Cladosporium?
	<i>Blastomyces dermatitidis</i>	.755		

*The *H. annosum* sequence was added to Genbank 10/96. It was not available on RDP at the time of this study, therefore sequences were compared using the GAP program of the Genetics Computing Group (GCG) package.

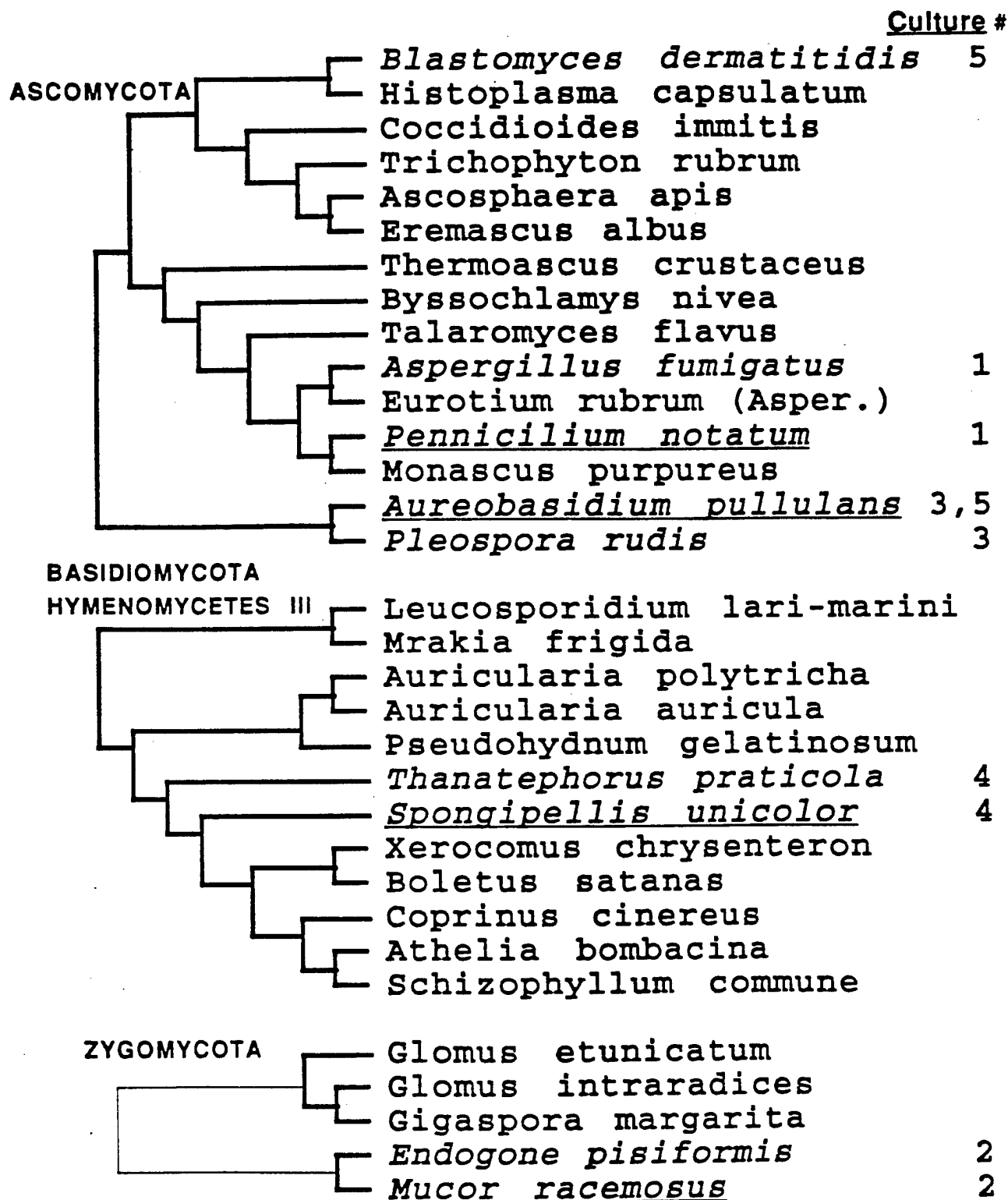


Figure 2. Phylogenetic Tree of Fungal SSU rDNA Sequences (provided by the Ribosomal Database Project, Maidak *et al.*, 1996). Branches without closest matching sequences have been omitted from the figure, but were included in the tree analysis. Closest matching sequences are underlined, next closest matches are italicized, and the stock cultures' number is listed next to each.

similarity rank of 0.881. Culture 3 had a characteristic yeast form, with some pseudomycelium also present. Conidia appeared to resemble *Torula* more than *Aureobasidium* in form. A sequence for the *Torula* SSU rDNA gene was not available on the RDP, but *Aureobasidium* was a close match with a Similarity Rank of 0.884. Culture 4 had previously been tentatively identified as *Heterobasidion annosum*, but no diagnostic morphological features were observed for the stock culture at the time of this study. The SSU rDNA sequence was highly related to *Spongipellis unicolor* (Similarity rank 0.807; GCG-GAP quality index 1010.7) and *Heterobasidion annosum*, a common airborne forest pathogen, was a close second, based on a GCG-GAP quality index of 1008.7. For culture 5, sequence comparisons were indeterminate, as the two closest matches were separated on the phylogenetic tree, and had a relatively low similarity rank (0.831 for *Aureobasidium pullulans* and 0.755 for *Blastomyces dermatitidis*). The culture resembled a *Cladosporium* sp., but directly observed characters were not sufficient to identify the culture with any confidence.

The fungal SSU rDNA sequences available through the ribosomal database project are displayed in Figure 2, arranged according to phylogenetic relationship. Some branches have been omitted due to lack of space, without influencing the arrangement of species. Closest matching sequences are underlined, while next closest sequences are italicized.

Molecular Markers of Cultures 1, 2, and 3

Restriction fragment length polymorphisms (RFLP's) of the SSU rRNA gene for three of the cultures were analyzed. In Figure 3, a gel of RFLP's with the restriction enzyme Cfo I shows a pattern of three bands (750 bp, 260 bp, 170 bp) for Culture 1 and 3, and a pattern of two bands (750 bp and 400 bp) for Culture 2. When the restriction enzyme Hpa II was used (figure 4), the RFLP pattern had three bands for Culture 1 and 3 (410 bp, 210 bp, and 90 bp) and Culture 2 had two bands (750 bp and 400 bp). While Cultures 1 and 3 are indistinguishable with these two enzymes, Culture 2 can be distinguished with either enzyme.

When genomic DNA extracts from different cultures were mixed before PCR amplification of the SSU gene, the effect of mixing varied. Lanes 2-4 and 6 of the gels in Figures 3 and 4 show the results of mixing gDNA extracts 1:1. The mixture of Culture 2 and 3 (lane 6) has bands from both cultures, while the mixture of Culture 1 and 3 (lane 3) reflects the presence of Culture 1 only. When gDNA extracts were mixed 1:100, the minor component could still be detected with some cultures (lane 11--Culture 1), while with other cultures the minor component was swamped out by the major component (lanes 10 and 12--Culture 2; lane 13--Culture 3).

Lane 1: Culture 1
 Lane 2: Culture 1 & 3 (1:1)
 Lane 3: Culture 1 & 2 (1:1)
 Lane 4: 1 & 2 & 3 (1:1:1)
 Lane 5: Culture 3
 Lane 6: 2 & 3 (1:1)
 Lane 7: Culture 2
 Lane 8: Culture 1 & (3) (1:100)
 Lane 9: Culture 3 & (1) (1:100)
 Lane 10: Culture 1 & (2) (1:100)
 Lane 11: Culture 2 & (1) (1:100)
 Lane 12: Culture 3 & (2) (1:100)
 Lane 13: Culture 2 & (3) (1:100)
 Lane 14: 100 bp DNA ladder

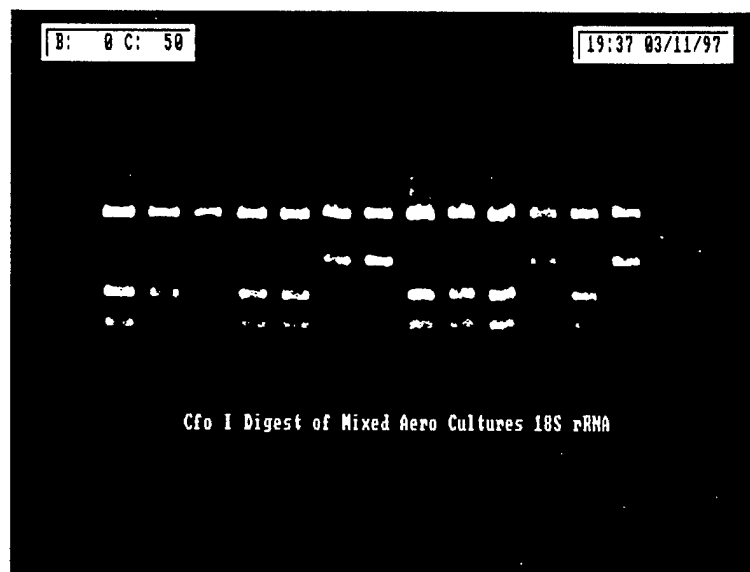
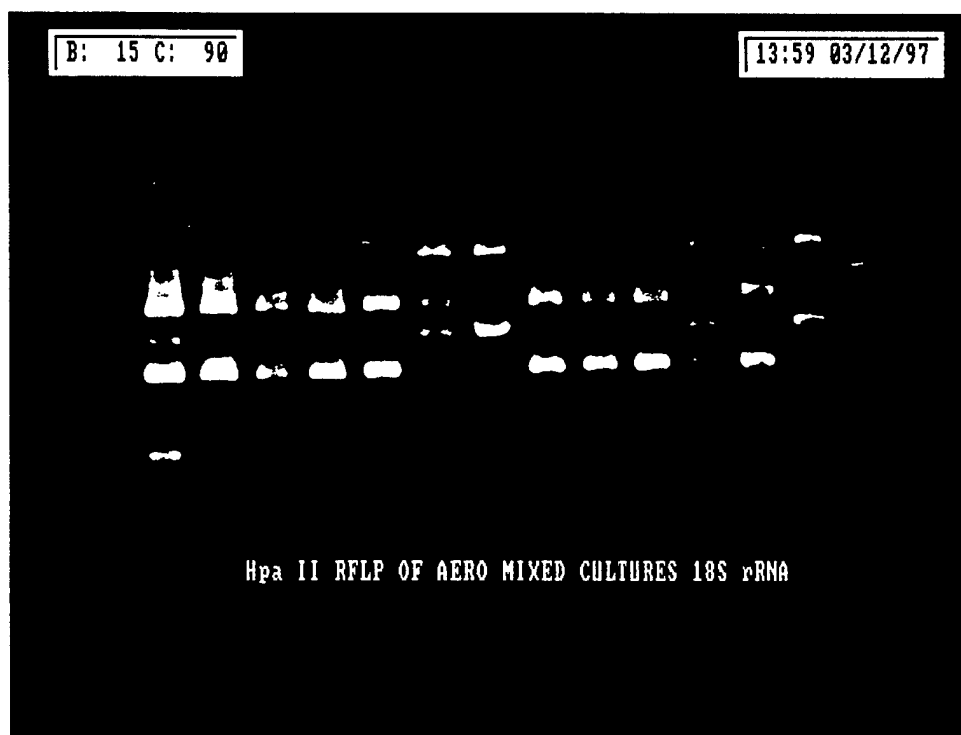


Figure 3. Gel of RFLP's of the SSU rDNA Gene Digested with Cfo I.
 Genomic DNA samples from stock cultures were diluted 1:1000 in water, then used for PCR directly, or mixed 1:1 or 1:100 with other stock cultures' gDNA.

Figure 4. Gel of RFLP's of the SSU rDNA Gene Digested with Hpa II.

Genomic DNA samples from stock cultures were diluted 1:1000 in water, then used for PCR directly, or mixed 1:1 or 1:100 with other stock cultures' gDNA.

Lane 1: Culture 1
Lane 2: Culture 1 & 3 (1:1)
Lane 3: Culture 1 & 2 (1:1)
Lane 4: 1 & 2 & 3 (1:1:1)
Lane 5: Culture 3
Lane 6: 2 & 3 (1:1)
Lane 7: Culture 2
Lane 8: Culture 1 & (3) (1:100)
Lane 9: Culture 3 & (1) (1:100)
Lane 10: Culture 1 & (2) (1:100)
Lane 11: Culture 2 & (1) (1:100)
Lane 12: Culture 3 & (2) (1:100)
Lane 13: Culture 2 & (3) (1:100)
Lane 14: 100 bp DNA ladder



DISCUSSION

Sequence Analysis

Of the five stock cultures that were selected for study, only one (*Mucor*) could be identified to genus with some degree of confidence. The similarity rank of 0.881 when comparing *Mucor racemosus* and the unknown sequence was high enough to indicate highly related sequences, consistent with both organisms being in the same genus. Direct observation of sporangia in light and scanning electron microscopy confirmed that the isolate was *Mucor*. It is important to note that relatively few sequences are available for zygomycetes (Figure 2), and therefore it was lucky that the *Mucor racemosus* sequence was available. The low resolution on the phylogenetic tree for this branch was reflected also in the low similarity rank of 0.408 for the second most similar organism, *Endogone pisiformis*.

Culture 3 had a high similarity rank of 0.884 to *Aureobasidium pullulans*. Unfortunately, this isolate could not be identified by direct observation in our stock cultures (possibly due to the long period in culture), and therefore it is impossible to evaluate whether or not the culture actually was in the genus *Aureobasidium*. It was an interesting coincidence that culture 5 was also most highly related to *Aureobasidium pullulans*, but with a lower similarity rank of only 0.831. This result emphasizes the importance of paying attention to the degree of similarity instead of merely identifying the most highly related organism. It was also interesting to note that culture 5 had as its next closest match *Blastomyces dermatitidis*, an organism which was on a distant branch from *Aureobasidium pullulans*. This was probably due to the relatively low similarity rank, and can be explained by the rapid decrease in reliability of the alignment as the similarity between the two compared sequences decreases.

Culture 4 was found to be most similar to *Spongipellis unicolor* (0.807), with *Heterobasidion annosum* a close second. The SSU rDNA sequence for *H. annosum* was not yet available on the RDP database, but was submitted to the Genbank database in October of 1996, therefore comparisons were performed using the GAP program of the Genetics Computing Group (GCG) software package (Table 1). Again, visual inspection of the stock culture at the time of DNA isolation did not yield a reliable identification, however this culture had originally been identified as *H. annosum*. It is curious that the similarity rank was quite low (probably just under 0.807), if the stock culture was indeed the same species as the one reported in Genbank. It is possible that the species *H. annosum*, as currently defined, could encompass a wide range of genetic types, or that our stock culture was either misidentified or replaced by a contaminant. To address this

question, further research could look at SSU rDNA sequences from well-identified *H. annosum* cultures.

Culture 1 had been identified as *Penicillium* sp., and had some characteristics of *Penicillium* such as the prodigious production of blue-green spores, however the conidiophore structure was not typical of *Penicillium*. This observation was reinforced by the relatively low similarity rank (0.749) between the stock culture and *Penicillium notatum*, the most closely related sequence in the RDP database.

The SSU rDNA gene appeared to be effective in some cases in identifying unknown stock cultures to the genus level, but the power of the approach was severely limited by lack of resolution in the phylogenetic tree of available known sequences for comparison. Until more sequences become available, it will be difficult to use this approach for any but the most common genera of fungi. However, the recent advent of easily accessible and complete databases like the ribosomal database project should encourage other researchers to contribute new SSU sequences. The addition of a *H. annosum* sequence to the database during the course of this study provides an example of the rapid rate of expansion of the database.

Molecular Markers for Detecting Previously Identified Organisms

Culture 1 and Culture 3 had identical RFLP patterns with both restriction enzymes that were used (Figures 3 and 4). This is not unexpected, since the SSU rDNA gene is quite highly conserved, resulting in similar RFLP patterns among genera that are not closely related. In future research, we plan to use a less highly conserved region of the ribosomal gene cluster, which should result in unique RFLP patterns for most genera of fungi. Specifically, the internal transcribed spacers (ITS-I and ITS-2, see Figure 1) have been used by researchers for molecular markers at the genus, species, or strain level (Gardes and Bruns, 1993).

It was possible to distinguish between Culture 2 and Cultures 1 and 3 using SSU rDNA RFLP's (Figures 3 and 4). This made it possible to examine the effect of mixing gDNA from different stock cultures, to mimic the effect of isolating gDNA from mixed samples of airborne fungal spores. In 1:1 mixtures, Culture 2 could be detected from mixtures with gDNA from Culture 3 (lane 6), but not from Culture 1 (lane 3). In 1:100 mixtures, Culture 2 could not be detected as a minor component (lanes 10 and 12). In contrast, Culture 1 could be detected both as a major component (100:1, lane 10) and as a minor component (1:100, lane 11) with Culture 2. These differences probably reflect variation in the efficiency of gDNA extraction from each stock culture. Culture 1 appeared to have either a more efficient gDNA extraction from the starting biomass, or more copies

of the rDNA gene in its genome; consequently it was more likely to "swamp out" the other organisms' gDNA in mixtures. Despite the limitation of not knowing the starting concentration of gDNA, these results indicate that PCR amplification could be able to detect SSU rDNA genes even from organisms which represent a minor component in the original fungal spore mixture.

In future research, we would like to attempt to amplify SSU rDNA genes from gDNA isolated from single airborne spores. Lee and Taylor (1990) reported successful amplification from single ascospores of *Neurospora tetrasperma*. It remains to be determined whether single spore amplification will work from conidia and yeast cells dispersed as airborne particles. We propose the following strategy for identifying airborne spores of interest. First, physical or biochemical methods would be used to detect the presence of unusual or interesting fungal spores. Second, gDNA could be obtained from a single spore, and the SSU rDNA gene could be sequenced, providing phylogenetic information about the most closely related known organism. Finally, RFLP's or other molecular markers could be used to detect the presence of that unique spore in gDNA isolated from samples of mixed fungal airborne spores from the environment.

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APPENDIX A

SEQUENCE OF CULTURES DATA

A.1: Sequence of Culture 1 (*Penicillium?*)

1 ATNACCANAC ANATCTAAGT ATAAGCAACT TGTACTGTGA AACTGCGAAT
51 GGCTCATTAAT ATCAGTTATC GTTTATTTGA TAGTACCTTA CTACATGGAT
101 ACCTGTGGTA ATTCTAGAGC TAATACATGC TAAAAACCCC GACTTCAGGA
151 AGGGGTGTAT TTATTAGATA AAAAACCAAC GCCCTTCGGG GCTCCTTGGT
201 GAATCATAAT AACTTAACGA ATCGCNTGGC CTTGCNCCGG CGATGGTTCA
251 TTCAAATTTT TGCCCTATCA ACTTTCGATG GTAGGATAGT GGCCTACCAT
301 GGTGGCANC GGNNNCGGGG AATTANGGTT CGATCCCGBA GAGGGAGCCT
351 GAGAAACGGC TACNACATCC AATGAAGGCA NCTGGCCNCA AATTTCCANT
401 CCCTATTCNG GGATGTAGTN ACAATAAATA CTGANNCTGG GCTCTTTTGG
451 GTCTCNTNNN TTGGANTTNA AANCTATTNTATCCCTTA ACGAGGAACA
501 ATTGGAGGGC AANTTTTGGN CCACCNACCC GGGGTAAATT CCCAGCTCCA
551 TANNGNAANA TAAAAGTTGT GCCATTTAAA AGGTTCGTAA GTGGACCTTG
601 GGTNTTGGCT GCGCGTCCCC CTCACCGCGA GNANTGGTCC GGCTGGACCT
651 TTCCTTNTGG GGAACCTCAT GGCCTTCACT GGCTGTGGGG GGAACCAGGA
701 CTTTTACTGT GAAAAATTA GAGTGTTCAG AGCAGGCCTT TGCTCGAATA
751 CATTAGCATG GAATAATAGA ATAGGACGTG TGGTCTATT TTGTTGGTTT
801 CTAGGACCGC CGTAATGATT AATAGGGATA GTCGGGGGCG TCAGTATTCA
851 GCTGTCAGAG GTGAAATTCT TGGATTTGCT GAAGACTAAC TACTGCGAAA
901 GCATTGCGCA AGGATGTTTT CATTAAATCAG GGAACGAAAG TTAGGGGATC
951 GAAGACGATC AGATACCGTC GTAGTCTTAA CCATAAACTA TGCCGACTAG
1001 GGATCGGACG GGTTCTATGA TGACCCGTTC GGCACCTTAC GAGAAATCAA
1051 ATTTTTGGTT CTGGGGGATG ATGTCGCANG GTNA

A.2: Sequence of Culture 2 (*Mucor?*)

1 TTNANGANTG ACGATGNAAG TATAAATAAA TTTATATTGT GAAACTGCCA
51 ATGGCTCATT AAATCAGTTA TGATCTACGT GACATATTTT TTTACTACTT
101 GGATAACCGT GGTAATTCTA GAGCTAATAC NTGCAAAAAA ACCCTGACTT
151 ACGAAAGGGT GCACTTATTA GATAAAGCCA ACGCTGGGTA AAACCAGTTT
201 CCCTTGGTGA TTCATAATAA TTTAGCGGAT CGCNTGGCCT TGTGCTAGCG
251 ACAGTCCACT CGATTTTCTG CCCTATCATG GTTGAGATTG TAAGATAGAG
301 GCTTACAANG CCTACAACGG GTANCGGGGA ATTAGGGTTC GATTCCGGAG
351 AGGGAGCCTG AGAAACGGCT ACCACNTCCA ANGAAGGCAG CTGCGCGCA
401 AATTACCCAA TCCCGACTCG GGGAGGTAGT GACAATAAAT AACAATGCAG
451 GGCCTTTAAG GTCTTGCAAT TGGAAATGAGT ACAATTTAAA TCCCTTAACG
501 AGGATCAATT GGAGGGCAAG TCTGGTGCCC AGCAGCCGCG GTAATTCCAG
551 CTCCCATAGC GTATATTAAA GTTGTTGCAG TTAAAACGTC CGTAGTCAAA
601 TTTTAGTCTT TAGATGAGGT GGCCTGGTCT TCATTGATCA AGCTCGCTTT
651 TATCGAGACT TTTTTTCTGG TTATGCTATG AATAGCTTCG GTTGTTTATA
701 GTCTCTAGCC AGATGATTAC CATGAGCAAA TCAGAGTGTT TAAAGCAGGC
751 TTTTAAGCTT GAATGTGTTA GCATGGAATA ATGAAATATG ACTTTAGTCC
801 CTATTTTCGTT GGTTCAGGAA CTTAAGTAAT GATGAATAGA AACGGTTGGG
851 GACATTTGTA TTTGGTCGCT AGAGGTGAAA TTCTTGGATT GACCGAAGAC
901 AACTACTGC GAAAGCATTT GATCCAGGAC GTTTTCATTG ATCAAGGTCT
951 AAAGTTAAGG GATCGAAGAC GATTAGATAC CGTCGTAGTC TTAACCACAA
1001 ACTATGCCGA CTAGAGATTG GGCTTGTTTA TTATGACTAG CTCAGCATCT
1051 TAGCGAAAGT AAATTTTTGG TTCTGGGGGG TGTNTAACAG GGTGNNNNNN
1101 NNN

A.3: Sequence of Culture 3 (*Aureobasidium?*)

1 C TTCAGGATT GACGGANGAA GGTGTGGCGC TNTTCGGTGA AACTGCGAAT
51 GGCTCATTA ATCAGTTATC GTTTATTTGA TAGTACCTTA CTA CTCTGGAT
101 AACCGTGGTA ATTCTAGAGC TAATACATGC TAAAAACCCC AACTTCGGAA
151 GGGGTGTATT TATTAGATAA AAAACCAACG CCCTTCGGGG CTCCTTGGTG
201 ATTCATAATA ACTAAACGAA TCGCATGGCC TTGCGCCGGC GATGGTTCAT
251 TCAAATTTCT GCCCTATCAA CTTTCGATGG TAGGATAGTG GCCTACCATG
301 GTATCAACNG GTAACGGGGA ATTAGGGTTC TATTCCGGAG AGGGAGCCTG
351 AGAAACGGCT ACCACATCCA AGGAAGGCAG CAGGCGCGCA AATTACCAAT
401 CCCGACACGG GGAGGTAGTG ACAATAAATA CTGATACAGG GCTCTTTTGG
451 GTCTTGTAAT TGAATGAGT ACAATTTAAT CCTTAAACGA GGAACAATTG
501 GAGGCAAGTC TGGTGCCAGC AGCCGCGGNA ATTCCAGCTC CCATTAGCGT
551 ATATTAAAGT TGTTCAGTT AAAAAGCTNC GTAGTTGAAC CTGGGCCTG
601 GCTGGCCGGT CCGCCTCACC GCGTGTANTG GTCCGGCCGG GCCTTTCCTT
651 CTGGGGAGCC GCATGCCCTT CACTGGGCGT GTCGGGGAAC CAGGACTTTT
701 ACTTTGAAAA AATTAGAGTG TTCAAAGCAG GCCTTTGCTC GAATACATTA
751 GCATGGAATA ATAGAATAGG ACGTGCGGTT CTATTTNGTT GGTTCCTAGG
801 ACCGCCGTAA TGATTAATAG GGATAGTCGG GGGCATCAGT ATTCAATTGT
851 CAGAGGTGAA ATTCTTGAT TTATTGAAGA CTA ACTACTG CGAAAGCATT
901 TGCCAAGGAT GTTTTCATTA ATCAGTGAAC GAAAGTTAGG GGATCGAAGA
951 CGATCAGATA CCGTCGTAGT CTTAACCATA AACTATGCCG ACTAGGGATC
1001 GGGCGATGTT ATCATNTGA TCGTTCGNCA CCNTACGAGA AATCAAATCT
1051 ACGGATCNGG TGATGNATCA CAGTTTCNNN NGN

A.4: Sequence of Culture 4 (*Heterobasidion annosum?*)

1 TNTTGGACCG ACANATCTAA GTATAAACAA GTTTGTACTG TGAAACTGCG
 51 AATGGCTCAT TAAATCAGTT ATAGTTTATT TGATGGTGCT TTGCTACATG
 101 GATAACTGTG GTAATTCTAG AGCTAATACA TGCAATCAAG CCCCAGCTTC
 151 TGGAAGGGGT GTATTTATTA GATAAAAAAC CAACGCGGTT CGCCGCTCCA
 201 TTGGTGATTC ATAATAACTT CTCNAATCGC ATGGCCTTGT GCCGGCGATG
 251 CTTCAATTCAA ATATCTGCCC TATCaACTTT CGATGGTAGG ATAGAGGCCT
 301 ACCATGGTTT CAACGGGTAA CGGGGAATNA GGGTTCGATT CCGGAcAGGG
 351 AGCCTGAAAA ACGGCTACCA CNTCCAAGGA AGGCNGCAGG CGCGCAAATT
 401 NCCCANTCCC GACCGGGGAG GTAGTGACAA TAAATAACAA TATAGGGCTC
 451 TTTCGGGTCT NATAATTGGA ATNAGTACAA TTTAAATCTC GAGGA
 501 ACAATTGGAG GGCAAGTCTG GTGCCAGCAG CCGCGGTAAT TCCAGCTCCA
 551 ATAGCGTATA TTAAAGTTGT TGCAGTTAAA AAGCTCGTAG TTGAACTTCA
 601 GGCCTGGCTG GCGGTCTGTC CTAACGGTAT GTACTGTCTG GCTGGGTCTT
 651 ACCTCTTGGT GAGCCGGCAT GCCCTTCACT GGGTGTGTCG GGAACCCAGG
 701 ACTTTTACCT TGAGAAAATT AGAGTGTTC AAGCAGGCTT ATGCCCCGAAT
 751 ACATTAGCAT GGAATAATAA AATAGGACGT GCGGTTCTAT TTTGTTGGTT
 801 TCTAGAGTCG CCGTAATGAT TAATAGGGAT AGTTGGGGGC ATTAGTATTC
 851 CGTTGCTAGA GGTGAAATTC TTGGATTTAC GGAAGACTAA CTACTGCGAA
 901 AGCATTTGCC AAGGATGTTT TCATTAATCA AGAACGAAGG TTAGGGGATC
 951 GAAAACGATC AGATACCGTT GTAGTCTTAA CAGTAAACTA TGCCGACTAG
 1001 GGATCGGGCG AANTCAATTN GATGTGTCGC TCGGCACCNN ACGAGAAATC
 1051 AAATCNCNGG NTCCCGTGNT NNNNATTCAT ATGCTNTTCC

A.5: Sequence of Culture 5 (*Cladosporium?*)

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1  AAAGATGANC GNCNNTCTAA GTATAAGCAA CTATACGGTG AAAC TGCGAA
51  TGGCTCATT AATCAGTTAT CGTTTATTTG ATAGTACCTT ACTACTTGGA
101 TAACCGTGGT AATTCTAGAG CTAATACATG CTAAAAACCT CGACTTCGGA
151 AGGGGTGTNT TTATTANATA AAAAACCAAT GCCCTTCGGG GCTCCTTGGT
201 GATT CATAAT AACTTAACGA ATCNCATGGC CTTGTGCCGG CGATGGTTCA
251 TTCAAATTC TGCCCTATCA ACTTTCGATG GTAGGATAGT GGCCTACCAT
301 GGTTC CAAC GGGTNACGGG GAATTAGGGT TCTATTCCGG ANANGGACCT
351 GAGAAACGGC TGCCACATCC AAGGAAGGCA GCAGGCGCGC AAATTACCCA
401 ATCCC GACAC GGGGAgGTag TGACAATAAA TACTGATACA GGGCTCTTTT
451 GGGTCTTGTA ATTGGAATGA NTACAATTTA AATCCCTTAA CGAgGAACAA
501 TTGGAgGGCA AGTCTGGTGC CAgCAGCCGC GGTAAATCCA GCTCCAATAg
551 CGTATATTAA AgTTGTTGCA GTTAAAAAGC TCgTagTTGA ACCTTGAGCC
601 TGGCTGGCCG GTCCGCCTCA CCGCGTGCAc TGGTCCGGCC GGGTTTTTCC
651 TTcTGGGGAG CCGCATGCCC TTCAcTGGGT GTGTCCGGGA ACCAGGACTT
701 TTACTTTGAA AAAATTAGAG GTTCAAAGC AGGCCTATGC TCGAATACAT
751 TAGCATGGAA TAATAGAATA GGACGTGTGG TTCTATTTTG TTGGTTTTCT
801 AGGACCGCCG TAATGATTAA TAGGGATAGT CGGGGGCATC AGTATTCAAT
851 TGTCAGAGGT GAAATTTCTT GGATTTATTG AAGACTAACT ACTGCGAAAG
901 CATTTGCCAA GGATGTTTTT ATTAATCAGT GAACGAAAGT TAGGGGATCG
951 AAGACGATCA GATACCGTCG TAGTCTTAAC CATAAACTAT GCCGANTAGG
1001 GATCGGGCGA TGNTATTTTT TTGACTCGCT CGGCACCTTA CGAGAAATCA
1051 AATCTTTGGT TCTGGGGGGT ATGTCGCAAG GTGAA

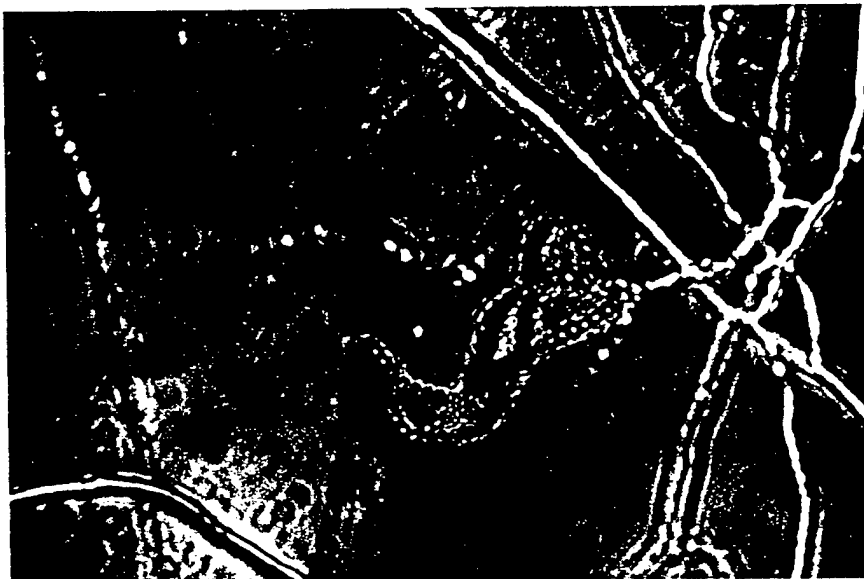
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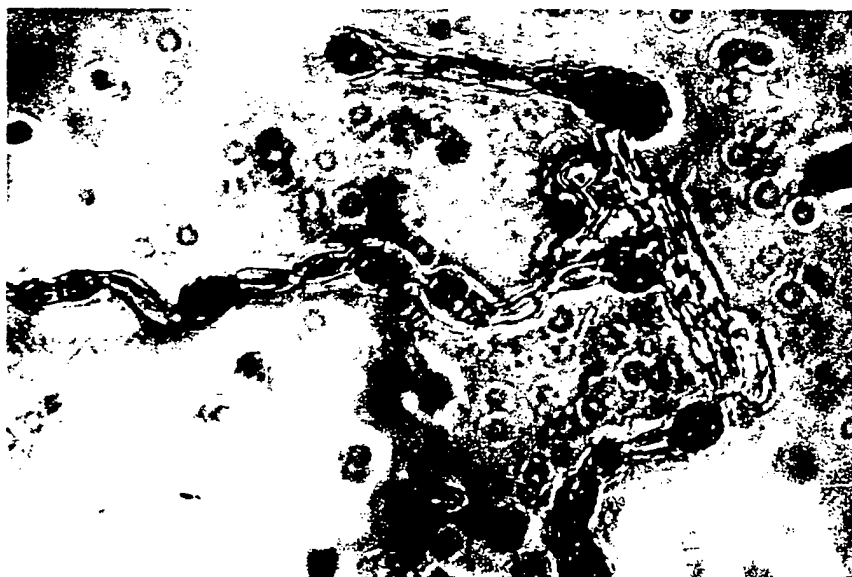
APPENDIX B

PICTURES OF STOCK CULTURES

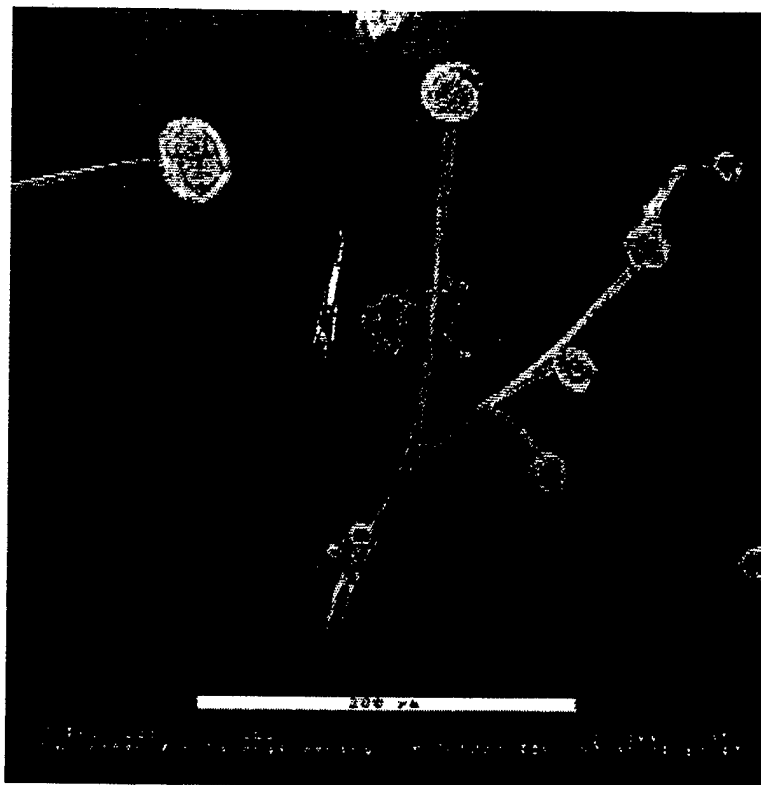
Culture 1: *Penicillium* (?), conidiophore and conidia in long chains, 400x.



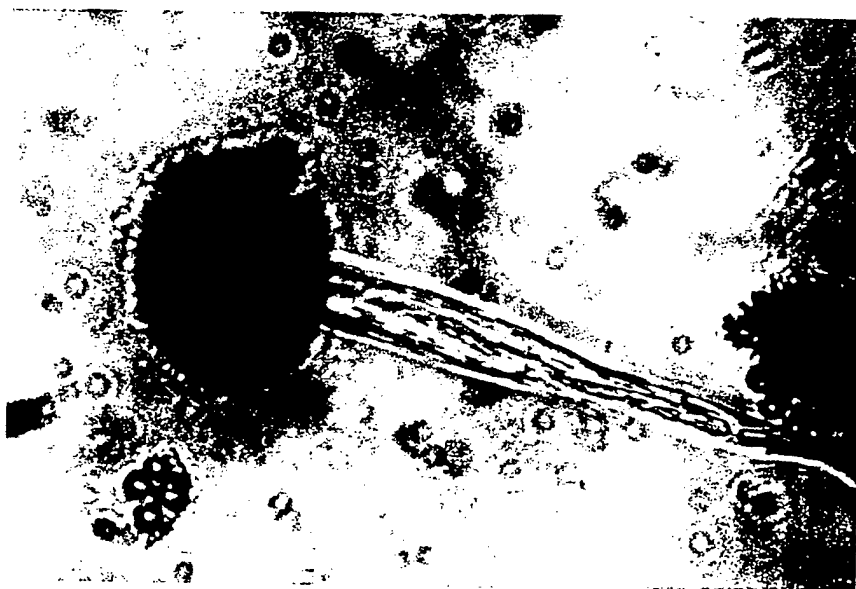
Culture 3: *Aureobasidium* (?), pseudomycelium and yeast growth form, dark conidia?, 400x.



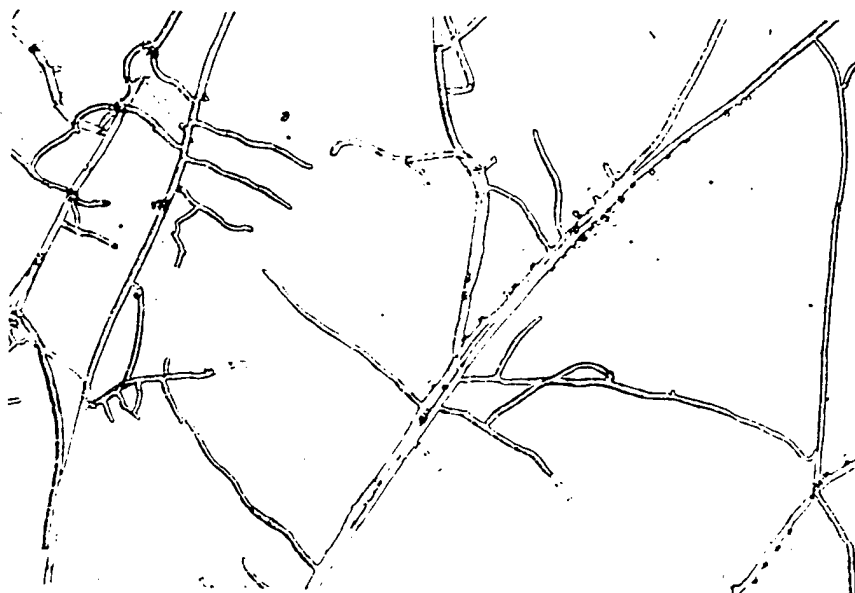
Culture 2: *Mucor*, branched sporangiophore and sporangia, environmental SEM image.



Culture 2: *Mucor*, single sporangiophore and sporangium, 400x light micrograph.



Culture 4: *Heterobasidion annosum* (?), 100x.



Culture 5: *Cladosporium* (?), conidiophore and dark-celled conidia?, 400x light micrograph.



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APPENDIX C

BUFFERS

2X CTAB Lysis Buffer:

100 mM Tris-Cl (pH 8.0)

1.4 M NaCl

20 mM EDTA

2.0% w/v CTAB (Hexadecyltrimethyl-ammonium bromide)

Wash Buffer:

76 % ethanol

10 mM NH₄OAc